

sequence listing.txt
SEQUENCE LISTING

<110> The University of York

<120> Expansin Polypeptides

<130> P102868WO

<140> PCT/GB04/004058

<141> 2004-09-23

<150> 0322317.9

<151> 2003-09-24

<160> 24

<170> PatentIn version 3.1

<210> 1

<211> 783

<212> DNA

<213> Craterostigma plantagineum

<400> 1

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tatggcggca gCGatgcgag cggcaccatg ggcggcgCGt gCGgctatgg caacctgtat      180
agccagggct atggcaccaa caccgcggcg ctgagcaccg cgctgtttta caacggcctg      240
agctgcggca gctgctttga aattaaatgc gCGagcagca ttagcggcg gggcaaatgg      300
tgcctgccgg gCGgcagcat taccgtgacc gCGaccaact tttgcccgcc gaacaacgCG      360
ctgccgaaca acgCGggcg gctggtgcaac cCGccgctgc agcattttga tctgagccag      420
ccggtgtttc agcatattgc gcagtatcgc gCGggcattg tgccggtgag ctatcgccgc      480
gtgCCgtgcc gccCGcgCG ggcattcgc tttaccatta acggccatag ctattttaac      540
ctggtgctga ttaccaacgt gggCGgcCG ggcgatgtgc atgcggtgag cattaaaggc      600
gcgaccaccg attggcagcc gatgagccgc aactggggcc agaactggca gagcaacgCG      660
aaccCGaacg gccagcgcct gagctttaaa gtgaccacca gCGatggccg caccctggtg      720
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<210> 2

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<212> PRT

<213> Craterostigma plantagineum

<400> 2

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sequence listing.txt

Thr Ser Ser Ser His Phe Ala Arg Ala Tyr Tyr Gly Gly Asp Gly Gly
 20 25 30
 Trp Thr Asp Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly
 35 40 45
 Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr
 50 55 60
 Gly Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu
 65 70 75 80
 Ser Cys Gly Ser Cys Phe Glu Ile Lys Cys Ala Ser Ser Ile Ser Gly
 85 90 95
 Gly Gly Lys Trp Cys Leu Pro Gly Gly Ser Ile Thr Val Thr Ala Thr
 100 105 110
 Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn Asn Ala Gly Gly Trp
 115 120 125
 Cys Asn Pro Pro Leu Gln His Phe Asp Leu Ser Gln Pro Val Phe Gln
 130 135 140
 His Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Tyr Arg Arg
 145 150 155 160
 Val Pro Cys Arg Arg Arg Gly Gly Ile Arg Phe Thr Ile Asn Gly His
 165 170 175
 Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp
 180 185 190
 Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met
 195 200 205
 Ser Arg Asn Trp Gly Gln Asn Gln Ser Asn Ala Asn Pro Asn Gly Gln
 210 215 220
 Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val Ser
 225 230 235 240
 Asn Asn Val Ala Pro Pro Asn Trp Ser Phe Gly Gln Thr Phe Ala Gly
 245 250 255
 Ala Gln Phe Asn
 260

sequence listing.txt

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 <213> Craterostigma plantagineum

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 aacggcctga cctgcggcgc gtgctatgaa ctgacctgca acaacgatcc gcgcggctgg 180
 tgcctgagcg gcaccattat ggtgaccgcg accaactttt gcccgccgaa cccgagcctg 240
 ccgaacgata acggcggctg gtgcaacccg ccgcgccagc attttgatct ggcggaaccg 300
 gcgtttctgc agattgcgca gtataaagcg ggcattgtgc cggtgacta tcgccgcgtg 360
 ccgtgccaga aaaaaggcgg cattcgcttt accattaacg gccatagctt ttttaacctg 420
 gtgctggtga ccaacgtggg cggcgtgggc gatgtgcata gcgtgagcat taaaggcagc 480
 aacggcggct ggcagccgct gagccgcaac tggggccaga actggcagag caacagctat 540
 ctgaacggcc agagcctgag ctttcaggtg accaccagcg atggccgcac cgtgaccagc 600
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<210> 4
 <211> 219
 <212> PRT
 <213> Craterostigma plantagineum

<400> 4

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 1 5 10 15

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 20 25 30

Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Thr Cys Gly Ala Cys
 35 40 45

Tyr Glu Leu Thr Cys Asn Asn Asp Pro Arg Gly Trp Cys Leu Ser Gly
 50 55 60

Thr Ile Met Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Pro Ser Leu
 65 70 75 80

Pro Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg Gln His Phe Asp
 85 90 95

Leu Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Lys Ala Gly Ile
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100		105		110
Val Pro Val Asn Tyr Arg Arg Val Pro Cys Gln Lys Lys Gly Gly Ile	115	120		125
Arg Phe Thr Ile Asn Gly His Ser Phe Phe Asn Leu Val Leu Val Thr	130	135	140	
Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser	145	150	155	160
Asn Gly Gly Trp Gln Pro Leu Ser Arg Asn Trp Gly Gln Asn Trp Gln	165	170	175	
Ser Asn Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Gln Val Thr Thr	180	185	190	
Ser Asp Gly Arg Thr Val Thr Ser Tyr Asp Val Ala Pro Arg Gly Trp	195	200	205	
Gln Phe Gly Gln Thr Phe Glu Gly Gly Gln Phe	210	215		

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tttaacaacg gcctggcgtg cggcagctgc tatcaggtgc gctgcgaagg cggcccgaaa	180
tggtgcgtgc gcggcggcga tcgcattatt accgtgaccg cgaccaactt ttgcccggcg	240
aactatgcgc tggcgaacga taacggcggc tggtgcaacc cgccgcgcca gcattttgat	300
atggcgagc cggcgtttgt gcgcattgcg cattatcgcg cgggcattgt gccgattagc	360
tatcgccgcg tgagctgcgt gaaaaaaggc ggcattcgcc tgaccattaa cggccatagc	420
tattttaacc tggtgctggt gagcaacgtg ggcggcagcg gcgatgtgca tgcggtgtgg	480
attaaaggca gcggcgggcg cccgtggcag gcgatgaccc gcaactgggg ccagaactgg	540
cagagcaaca gctatctgga tggccagagc ctgagcttta ttgtgcgcgc gggcgatggc	600
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<210> 6

sequence listing.txt

<211> 224

<212> PRT

<213> Craterostigma plantagineum

<400> 6

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1 5 10 15

Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn
20 25 30

Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly
35 40 45

Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg
50 55 60

Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro
65 70 75 80

Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg
85 90 95

Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr
100 105 110

Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys
115 120 125

Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu
130 135 140

Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp
145 150 155 160

Ile Lys Gly Ser Gly Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp
165 170 175

Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser
180 185 190

Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Asp Ile
195 200 205

Val Pro Arg Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Pro Gln Phe
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<210> 7

sequence listing.txt

<211> 8
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 <213> Craterostigma plantagineum

<400> 7

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 <223> any nucleotide base

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sequence listing.txt

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sequence listing.txt

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sequence listing.txt

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23